include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are available, for example, on the Internet. Additional tools and software for ORF analysis include GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN. Open reading frames and portions of open reading frames may be identified in the polynucleotides of the present invention. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified. Thus, open reading frames encoding polypeptides may be identified using the polynucleotides of the present invention.--

B2 cont.

Replace the paragraph beginning on page 18, line 30, with the following amended paragraph:

--Polynucleotide and polypeptide sequences may be aligned, and percentage of identical residues in a specified region may be determined against another polynucleotide or polypeptide sequence, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. Polynucleotides may also be analyzed using the BLASTX algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. The similarity of polypeptide sequences may be examined using the BLASTP algorithm. The BLASTN, BLASTX and BLASTP programs are available on the NCBI anonymous FTP server under /blast/executables, and from the National Center for Biotechnology Information (NCBI) National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894, USA. The BLASTN algorithm Version 2.0.4 [Feb-24-1998] and Version 2.0.6 [Sept-16-1998], set to the default parameters described in the documentation and distributed with the algorithm, are preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including

B3

B3 cont. BLASTN, BLASTP, and BLASTX, is described at NCBI's Internet website and in the publication of Altschul et al., *Nucleic Acids Res.* 25:3389-3402, 1997.--

Replace the paragraph beginning on page 19, line 19, with the following amended paragraph:

B4 --The computer algorithm FASTA is available on the Internet, and from the University of Virginia by contacting David Hudson, Assistance Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA. Version 2.0u4 [February 1996], set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of variants according to the present invention. The use of the FASTA algorithm is described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson, *Methods in Enzymol.* 183:63-98, 1990.--

Replace the paragraph beginning on page 23, line 25, with the following amended paragraph:

B5 --In certain embodiments, the DNA constructs of the present invention include an open reading frame coding for at least a functional portion of a polypeptide of the present invention or a variant thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for regulating gene expression, *i.e.*, the portion of the molecule that is capable of binding to, or interacting with, the promoter of the gene to be expressed. The DNA-binding domain(s) for certain of the inventive polypeptides are identified below in Table 2. These DNA binding domains were identified using PROSITE 15.0 pattern or profile sequences as listed in the PROSITE database. PROSITE is available on the Internet and its use is described in Hofman et al., *Nucleic Acids Res.* 27:215-219, 1999; and in Bairoch, *Nucleic Acids Res.* 20:Suppl.2013-2018, 1992.--

Replace the paragraph beginning on page 32, line 22, with the following amended paragraph:

B6 --In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in